

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Ile Gly His Asp Cys Ala His  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Val Val Gly His Asp Cys Gly His  
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

His Asn Ala His His  
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (peptide)

00934254-091937

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

His Asn Tyr Leu His His  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

His Arg Thr His His  
1 5

08304254-091997  
(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Arg Arg His His  
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

His Asp Arg His His  
1 5

67

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

His Asp Gln His His  
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

His Asp His His His  
1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Asn His His His  
1 5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Phe Gln Ile Glu His His  
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

His Gln Val Thr His His  
1 5

00974254-091997  
266150-4524560  
(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

His Val Ile His His  
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

His Val Ala His His  
1 5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His Ile Pro His His  
1 5

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

His Val Pro His His  
1 5

(3) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1702 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 48..1406

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 48..1406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCCCAAAAT TTTCATTGTT CTCCATCTGG ACCACAGCAT CCACACA ATG GAG GGC  
Met Glu Gly  
1

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GAA GCT AAG AAG TAT ATC ACG GCG GAG GAC CTC CGC CGC CAC AAC AAG  
Glu Ala Lys Lys Tyr Ile Thr Ala Glu Asp Leu Arg Arg His Asn Lys  
5 10 15

104

TCC GGC GAT CTC TGG ATC TCC ATC CAG GGC AAG GTC TAC GAC TGC TCT

152

70

08924254 0091997 2661602 45242680

Ser 20	Gly	Asp	Leu	Trp	Ile 25	Ser	Ile	Gln	Gly	Lys 30	Val	Tyr	Asp	Cys	Ser 35	
CGG	TGG	GCG	GCG	GAG	CAC	CCC	GGC	GGC	GAG	GTC	CCG	CTC	CTC	AGT	CTG	200
Arg	Trp	Ala	Ala	Glu 40	His	Pro	Gly	Gly	Glu 45	Val	Pro	Leu	Leu	Ser 50	Leu	
GCC	GGC	CAG	GAC	GTC	ACC	GAC	GCC	TTC	ATT	GCG	TAC	CAC	CCG	GGC	ACG	248
Ala	Gly	Gln	Asp 55	Val	Thr	Asp	Ala	Phe 60	Ile	Ala	Tyr	His	Pro	Gly	Thr	
GCG	TGG	CGG	CAT	CTG	GAT	CCG	CTC	TTC	ACC	GGC	TAC	TAC	TAC	CTC	AAG	296
Ala	Trp	Arg 70	His	Leu	Asp	Pro	Leu 75	Phe	Thr	Gly	Tyr	Tyr 80	Tyr	Leu	Lys	
GAC	TTC	GAA	GTG	TCG	GAG	ATC	TCC	AAG	GAC	TAC	CGG	AGG	CTT	TTG	AAC	344
Asp	Phe 85	Glu	Val	Ser	Glu 90	Ile	Ser	Lys	Asp	Tyr	Arg 95	Arg	Leu	Leu	Asn	
GAG	ATG	TCG	CGG	TCC	GGG	ATC	TTC	GAG	AAG	AAG	GGC	CAC	CAC	ATC	ATG	392
Glu	Met	Ser	Arg	Ser	Gly 105	Ile	Phe	Glu	Lys	Lys 110	Gly	His	His	Ile	Met 115	
TGG	ACG	TTC	GTC	GGC	GTT	GCG	GTC	ATG	ATG	GCG	GCA	ATC	GTC	TAC	GGC	440
Trp	Thr	Phe	Val	Gly 120	Val	Ala	Val	Met	Met 125	Ala	Ala	Ile	Val	Tyr	Gly 130	
GTG	CTG	GCG	TCG	GAG	TCC	GTC	GGA	GTT	CAC	ATG	CTC	TGC	GGC	GCA	CTG	488
Val	Leu	Ala	Ser 135	Glu	Ser	Val	Gly	Val 140	His	Met	Leu	Cys	Gly 145	Ala	Leu	
CTG	GGC	TTG	CTG	TGG	ATC	CAA	GCC	GCG	TAT	GTG	GGC	CAT	GAC	TCC	GGC	536
Leu	Gly	Leu 150	Leu	Trp	Ile	Gln	Ala 155	Ala	Tyr	Val	Gly	His 160	Asp	Ser	Gly	
CAT	TAC	CAG	GTG	ATG	CCA	ACC	CGT	GGA	TAC	AAC	AGA	ATC	ACG	CAA	CTC	584
His	Tyr 165	Gln	Val	Met	Pro	Thr 170	Arg	Gly	Tyr	Asn	Arg 175	Ile	Thr	Gln	Leu	
ATA	GCA	GGC	AAC	ATC	CTA	ACC	GGA	ATC	AGC	ATC	GCG	TGG	TGG	AAG	TGG	632
Ile	Ala	Gly	Asn	Ile	Leu 185	Thr	Gly	Ile	Ser	Ile 190	Ala	Trp	Trp	Lys	Trp 195	
ACC	CAC	AAC	GCC	CAC	CAC	CTC	GCC	TGC	AAC	AGC	CTC	GAC	TAC	GAC	CCC	680
Thr	His	Asn	Ala 200	His	His	Leu	Ala	Cys	Asn 205	Ser	Leu	Asp	Tyr	Asp 210	Pro	
GAC	CTC	CAG	CAC	ATC	CCC	GTA	TTC	GCC	GTC	TCC	ACC	CGA	CTC	TTC	AAC	728
Asp	Leu	Gln	His 215	Ile	Pro	Val	Phe	Ala 220	Val	Ser	Thr	Arg	Leu 225	Phe	Asn	
TCC	ATC	ACC	TCG	GTC	TTC	TAT	GGC	CGA	GTC	CTG	AAA	TTC	GAC	GAA	GTG	776
Ser	Ile	Thr 230	Ser	Val	Phe	Tyr	Gly 235	Arg	Val	Leu	Lys	Phe 240	Asp	Glu	Val	

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GCA Ala	CGG Arg 245	TTC Phe	CTA Leu	GTC Val	AGC Ser	TAC Tyr 250	CAG Gln	CAC His	TGG Trp	ACC Thr	TAC Tyr 255	TAC Tyr	CCG Pro	GTC Val	ATG Met	824
ATC Ile 260	TTC Phe	GGC Gly	CGA Arg	GTC Val	AAC Asn 265	CTC Leu	TTC Phe	ATC Ile	CAG Gln	ACC Thr 270	TTT Phe	TTA Leu	TTG Leu	CTC Leu	CTC Leu 275	872
ACC Thr	AGG Arg	CGC Arg	GAC Asp	GTC Val 280	CCT Pro	GAC Asp	CGC Arg	GCT Ala	CTA Leu 285	AAC Asn	TTA Leu	ATG Met	GGT Gly	ATC Ile 290	GCG Ala	920
GTT Val	TTC Phe	TGG Trp	ACG Thr 295	TGG Trp	TTC Phe	CCG Pro	CTC Leu	TTC Phe 300	GTA Val	TCT Ser	TGT Cys	CTC Leu	CCG Pro 305	AAC Asn	TGG Trp	968
CCT Pro	GAA Glu	CGG Arg 310	TTC Phe	GGG Gly	TTC Phe	GTC Val	CTC Leu 315	ATC Ile	AGC Ser	TTT Phe	GCG Ala	GTC Val 320	ACG Thr	GCG Ala	ATC Ile	1016
CAG Gln	CAC His 325	GTC Val	CAG Gln	TTC Phe	ACG Thr	CTC Leu 330	AAC Asn	CAC His	TTC Phe	TCC Ser	GGC Gly 335	GAC Asp	ACA Thr	TAC Tyr	GTG Val	1064
GGC Gly 340	CCC Pro	CCC Pro	AAG Lys	GGC Gly	GAC Asp 345	AAC Asn	TGG Trp	TTC Phe	GAG Glu	AAG Lys 350	CAG Gln	ACG Thr	AAA Lys	GGG Gly	ACG Thr 355	1112
ATC Ile	GAT Pro	ATC Ile	ACG Thr	TGC Cys 360	CCA Pro	CCG Pro	TGG Trp	ATG Met	GAC Asp 365	TGG Trp	TTC Phe	TTT Phe	GGT Gly	GGG Gly 370	CTG Leu	1160
CAG Gln	TTC Phe	CAG Gln	TTG Leu 375	GAG Glu	CAC His	CAC His	TTG Leu	TTC Phe 380	CCT Pro	AGG Arg	CTG Leu	CCG Pro	CGT Arg 385	GGG Gly	CAG Gln	1208
CTT Leu	AGG Arg	AAG Lys 390	ATT Ile	GCG Ala	CCC Pro	TTG Leu	GCT Ala 395	CGG Arg	GAC Asp	TTG Leu	TGT Cys	AAG Lys 400	AAG Lys	CAC His	GGG Gly	1256
ATG Met	CCG Pro 405	TAT Tyr	AGG Arg	AGC Ser	TTC Phe	GGG Gly 410	TTT Phe	TGG Trp	GAC Asp	GAC Asp	GCT Ala 415	AAT Asn	GTC Val	AGG Arg	ACA Thr	1304
ATT Ile 420	CGG Arg	ACG Thr	CTG Leu	AGG Arg	ASP Gat 425	GCG Ala	GCG Ala	GTT Val	CAG Gln	GCG Ala 430	CGT Arg	GAC Asp	CTT Leu	AAT Asn	TCG Ser 435	1352
GCC Ala	CCG Pro	TGC Cys	CCT Pro	AAG Lys 440	AAA Lys	CTT Leu	GGG Gly	TAT Tyr	GGG Gly 445	GAA Glu	GCT Ala	TAT Tyr	AAC Asn	ACC Thr 450	CAT His	1400
GGT Gly	TGA *	TTGTGTTT	GTGTGTGGG	TTGGAGGATC	TTCTATTAT	TGATTTATGT										1456

CCACAATATT GAACTGAATA ACCATGGAAG GCACCTACGTT CAGCTTAACT TTGCTTAACT	1516
TTGCTAGCTG GTTGCGTTCC CTTGTTGGGG GCAAGTGCA GTATTTATTT TCTTATCCCA	1576
TGTACTTTTT GATTATTGTT CTTATTCGTA TCATAAATAA TTTATTATTG ATTAATTTTT	1636
GTTGTAGTTG GGTGTCTATA GCAAGTTTAT AATACTGAGA TATATTTTTT TGGTAAAAAA	1696
AAAAAA	1702

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Glu	Gly	Glu	Ala	Lys	Lys	Tyr	Ile	Thr	Ala	Glu	Asp	Leu	Arg	Arg	
1				5					10					15		
His	Asn	Lys	Ser	Gly	Asp	Leu	Trp	Ile	Ser	Ile	Gln	Gly	Lys	Val	Tyr	
			20					25					30			
Asp	Cys	Ser	Arg	Trp	Ala	Ala	Glu	His	Pro	Gly	Gly	Glu	Val	Pro	Leu	
		35					40					45				
Leu	Ser	Leu	Ala	Gly	Gln	Asp	Val	Thr	Asp	Ala	Phe	Ile	Ala	Tyr	His	
	50				55						60					
Pro	Gly	Thr	Ala	Trp	Arg	His	Leu	Asp	Pro	Leu	Phe	Thr	Gly	Tyr	Tyr	
65					70				75					80		
Tyr	Leu	Lys	Asp	Phe	Glu	Val	Ser	Glu	Ile	Ser	Lys	Asp	Tyr	Arg	Arg	
			85						90					95		
Leu	Leu	Asn	Glu	Met	Ser	Arg	Ser	Gly	Ile	Phe	Glu	Lys	Lys	Gly	His	
		100						105					110			
His	Ile	Met	Trp	Thr	Phe	Val	Gly	Val	Ala	Val	Met	Met	Ala	Ala	Ile	
	115						120					125				
Val	Tyr	Gly	Val	Leu	Ala	Ser	Glu	Ser	Val	Gly	Val	His	Met	Leu	Cys	
	130				135						140					
Gly	Ala	Leu	Leu	Gly	Leu	Leu	Trp	Ile	Gln	Ala	Ala	Tyr	Val	Gly	His	
145					150					155					160	
Asp	Ser	Gly	His	Tyr	Gln	Val	Met	Pro	Thr	Arg	Gly	Tyr	Asn	Arg	Ile	
			165						170				175			



Thr Gln Leu Ile Ala Gly Asn Ile Leu Thr Gly Ile Ser Ile Ala Trp  
 180 185 190  
 Trp Lys Trp Thr His Asn Ala His Leu Ala Cys Asn Ser Leu Asp  
 195 200 205  
 Tyr Asp Pro Asp Leu Gln His Ile Pro Val Phe Ala Val Ser Thr Arg  
 210 215 220  
 Leu Phe Asn Ser Ile Thr Ser Val Phe Tyr Gly Arg Val Leu Lys Phe  
 225 230 235 240  
 Asp Glu Val Ala Arg Phe Leu Val Ser Tyr Gln His Trp Thr Tyr Tyr  
 245 250 255  
 Pro Val Met Ile Phe Gly Arg Val Asn Leu Phe Ile Gln Thr Phe Leu  
 260 265 270  
 Leu Leu Leu Thr Arg Arg Asp Val Pro Asp Arg Ala Leu Asn Leu Met  
 275 280 285  
 Gly Ile Ala Val Phe Trp Thr Trp Phe Pro Leu Phe Val Ser Cys Leu  
 290 295 300  
 Pro Asn Trp Pro Glu Arg Phe Gly Phe Val Leu Ile Ser Phe Ala Val  
 305 310 315 320  
 Thr Ala Ile Gln His Val Gln Phe Thr Leu Asn His Phe Ser Gly Asp  
 325 330 335  
 Thr Tyr Val Gly Pro Pro Lys Gly Asp Asn Trp Phe Glu Lys Gln Thr  
 340 345 350  
 Lys Gly Thr Ile Asp Ile Thr Cys Pro Pro Trp Met Asp Trp Phe Phe  
 355 360 365  
 Gly Gly Leu Gln Phe Gln Leu Glu His His Leu Phe Pro Arg Leu Pro  
 370 375 380  
 Arg Gly Gln Leu Arg Lys Ile Ala Pro Leu Ala Arg Asp Leu Cys Lys  
 385 390 395 400  
 Lys His Gly Met Pro Tyr Arg Ser Phe Gly Phe Trp Asp Asp Ala Asn  
 405 410 415  
 Val Arg Thr Ile Arg Thr Leu Arg Asp Ala Ala Val Gln Ala Arg Asp  
 420 425 430  
 Leu Asn Ser Ala Pro Cys Pro Lys Lys Leu Gly Tyr Gly Glu Ala Tyr  
 435 440 445  
 Asn Thr His Gly \*  
 450